

query (SEQ ID NO:1)  
sequence1 (SEQ ID NO:2)  
sequence2 (SEQ ID NO:3)  
sequence3 (SEQ ID NO:4)  
sequence4 (SEQ ID NO:5)  
sequence5 (SEQ ID NO:6)  
sequence6 (SEQ ID NO:7)  
sequence7 (SEQ ID NO:8)

LVAFADFG-SVTFTNAEATSGGSTVGPSDATVMDIEQDGSQLTETSGDS-VTV  
LVAFADFG-SVTFTNAEATSGGSTVGPSDATVMDIEQDGSQLTETSGDS-VTV  
LVPFANFG-TVTFTGAEATTSSGTVTAADATLIDIEQNGEVLTSGST-VTV  
LVQFANFG-TVTFTGASATQNGESVGVTGAQIIDLQQN-SVLTSGSTSSNS-VTV  
LVNFADFD-TVTFKDCSPSVSG-----STIVDIROQSLEVTECSTTGTTVTC  
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC  
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC  
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC

**FIGURE 1**

>P1;1b4k

structureX:1b4k: 10 :A : 335 :A :  
YPYTRLRRNRRDDFSRRLVRENVLTVDDLILPVFVLGVNQRESIPSPMPGVERLSIDQLLIEAE  
EWVALGI PALALFPVT : PVEKKSLDAEAYNPEGIAQRATRALRERFPELGI ITDVALDPFTTH  
GQDGILDDDGYVLNDVSIDVLVRQALSHAEAGAQVVAPSDMMGRIGAIREALESAG : HTNVRI  
MAYSAKYASAYYGPFRDAVGSASN LGKGNKATYQMDPANSDEALHEVAADLAEGADMVMVKPGM  
PYLDIVRRVK : DEFRAPTFVYQVSGEYAMHMGAIQNGWLAE : SVILESLTAFKragADGILTYF  
AKQAAEQLRR\* (SEQ ID NO:9)

>P1;SC001

sequence:SC001: 13 : : 340 :  
EISSVLAGGYNHPLLROWQSERQLTKNMLIFPLFISDNPDDTEIDSLPNINRIGVNRKDYLK  
PLVAKGLRSVILFGVPLIPGTKDGVTAADDPAGPVIQGIKFIREYFPELYIICDVCLCEYTS  
GHCGVLYDDGTINRERSVSRLAAVAVNYAKAGAHCVAPSMDIDGRIRDIKRGLINANLAHKT  
LSYAAKFSGNLYGPFRDAACSA : PSNGDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPST  
FYLDIMRDASEICKDLPICAYHVSGEYAMLHAAAEKGVVDLKTIAFESHQGFLRAGARLIITYL  
APEFLDWLDE\* (SEQ ID NO:10)

**FIGURE 17**

>P1;1a28  
structureX: 1a28A : 701 : : 915 : :  
AGHDNTKPDTSSSLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFLGWR SYKHVS  
GQMLYFAPDLILNEQRMKESSFYSLCLTMW-QIPQEFVKLQVSQEEFLCMKVLLLNTI-PLEGRLRSQTQFE  
EMRSSYIRELIKAIIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRLSVEFPEMMSEVIA  
A\* (SEQ ID NO:11)  
>P1;gi7766906  
sequence: gi7766906 : 27 : : 233 :  
EANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSSELPLDDQVILLRAGWNELLIASASHRSIA--V  
KDGILLATGLHVHRNSAHSAGVGAI FDRVLTELVSKMRDMQMDKTELGCLRAIVLFNPDS--KGLSNPAEVE  
ALREKVYASLEAYCKHKYP--EQPGRFAKLLRLPALRSIGLKCLEHLFF-FKLIGDT--PIDTFLMEMLE  
A\* (SEQ ID NO:12)

**FIGURE 20**

>P1;1a28  
structureX: 1a28A : 682 : : 921 : :  
QLIPPLINLLMSIEPDVIYAGHDNTKPDTSLLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQY  
SWMSLMVFGLGWRSYKHVGQMLYFAPDLILNEQRMKE-SSFYSLCLTMWQIPQEfvKLQVSQEEFLCMKVL  
LLLNTIPLEGRLR---SQTQFEEMRSSYIRELIKAIQLRKQGVVSSQRFYQLTKLLDNLHDLVKQLHL  
YCLNTFIQSRALSVEFPEMMSEVIAAQLPKIL\* (SEQ ID NO:13)  
sequence: gi3659931 : 14 : : 254 :  
LTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQVHLLEC  
AWLEILMIGLVWRSMEHP--GKLLFAPNLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSI  
ILLNSGVYTFSLSTLKSLEEKDHIIHRVLDKITDTLIHLMAKAGLTLQQQHERLAQLLLILSHIRHMSNKGME  
HLYSMKCKN--VVPLYDLLLEMLD-AHR-LH\* (SEQ ID NO:14)

FIGURE 24

>P1;1c3w  
structureX: 1c3wA : 5 : : 231 : :  
TGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGE--  
QN---PIYW-ARYADWLFTTPLLLALLVDADQGTILALVGADGIMIGTGLVGALTGVY--S--YRFVW  
WAISTA-AMLYIILYVLFVGF----SMRPE-VA-STFKVLRNVTVVLWSAYPVVWLIGSEG---AGI---V  
PLNIETLLFMVL-DVSAKVGFGILLRSRAIFG\* (SEQ ID NO:15)  
>P1;1e12A  
sequence: 1e12A : 4 : : 236 :  
ENALLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRLIWGATLMIPLVSISYYLGLLSGLTVGMIEMPAGHA  
LAGEMVRSQW-GRYLTWALSTPMILLALGLLADVDLGSLEFTVIAADIGMCVTGLAAAMTTS---ALLFRWAF  
YAISCA-FFVVVLSALVTDWAASASSAGT--A--EIFDTLRVLTVVWLGYPIVWAVGV-----EGLALVQ  
SVGATSWAYSVL-DVFAKYVFAFILLRWVANNE\* (SEQ ID NO:16)

**FIGURE 27**

>P1;1f88  
structureX: 1f88A : 37 : : 308 : :  
FSMLAAYMFLIMLGFPINFLTLVTVQHKKLRT----PLNYILLNLAVALDFMVFGGFTTLYTSLHGYF  
VFGPTGCNLEGFFATLGGEIALWSLVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGW  
SRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVHFIIPLIVIFFCYGQLVFTV-KEAAASATTQKAEKEV  
TRMVIIMVIAFLICWL PYAGVAFYIFTHQGSDFGPIFMTI PAFFAKTSAVYNPVIYIM\* (SEQ ID NO:17)  
>P1;1c3wA  
sequence: 1c3wA : 2 : : 215 : GRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYA-  
ITTLVPAIAFTMYLSMLLGYGLTMVP-FGGEQ  
-NPI-YWARYADWLFTPLLLLALLVDA-----D----QGTILALVGADGIMIGTGLVGAL-----  
TKVY-----SY-----RFVWWAISTAAMLYILYVLFFGFSMR--PEV-----ASTFKVL  
RNVTVVVLWSAYPVVWLIGSEGAGI-----VPLNI--ETLLFMVLDVSAKVGFLILL\* (SEQ ID NO:18)

**FIGURE 29**

>P1;6prc  
structureX: 6prcL : 14 : : 258 : : GTLIGGDLFDWFVGPYFVGFFGVSAIFFIFLGVSLIGYAASQG-P---  
---TW-DPFAISINPPDLKYGLG  
A-APLLEGGFWQAITVCALGAFISWMLREVEISRKLIGIGWHVPLAFCVP1FMFCVLQVFRPLLLGSWGHAFP  
YGILSHLDWVNNFGYQYLNWHYNPGHMSSVSFLFVNAMALGLHGGLILSVANP-GD-----GD-----  
-KVKTA-EHENQYFRDVVGYSIGALSIHRLGLFLASNIFLTGAFGTIASGPFWTRG\* (SEQ ID NO:19)  
>P1;6prcM  
sequence: 6prcM : 34 : : 292 :  
YSYWLKGKIGDAQIGPIYLGASGIAAAFAFGSTAILIILFNMAAEVHFDPQLQFFR--QFFWLGLYPPKAQYGMG  
I-PPLHDGGWWLMAGLFMTLSLGSWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLGSWSEGVP  
FGIWPHIDWLTAFSIRYGNFYYCPWHGFSIGFAYGCGLLFAAHGATILAVARFG-----GDREIEQITDRG  
T--AV--ERAALFWRWTFIGFNATIESVHRWGWFSLMVMVSASVGILLTGTFVDNW\* (SEQ ID NO:20)

**FIGURE 31**

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>P1;1qj8
structureX: 1qj8A : 4 : : 148 : :
TVTGGYAQSDAQGQM-NKMGGFNLKYRYEEDNSPLGVIGSFTYTE-K--SRTASSGDYN-KNQYYGITAGPA
YRINDWASIYGVVGVGYGFQTTTEYPTYK-NDTSYGFSYGAGLQFNPMENVALDFSYEQRIRS-----
--VDVGTWIAGVGYRF* (SEQ ID NO:21)
>P1;1bxwA
sequence: 1bxwA : 19 : : 171 :
YHDTGLINNN--GPTHENKLGAGAFGGYQV-NPYVGFEMGYDWL--GRMPYKGSVENGAYKAQGVQLTAKLG
YPIITDDLDIYTRLGGMVWRADTY-SNVYGKNHTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGT
RP-DNGMLSLGVSYRF* (SEQ ID NO:22)
```

**FIGURE 33**

>P1;2por  
structureX: 2por : 1 : : 301 :  
EVKLSGDARMGVMYNGDD--WNFSSRSRVLFTMSGTTDSGLEFGASFKAHESVG-----AETGEDGTV  
FLSG-AFGKIEMGDALGASEALFGD--LYEVGYTDLDRGGNDIPYL-----TGDERLTAEDNPVLLYTY-  
SA----GAFSVAASMS--DGKV-----GETSED-----DAQ---EMAVAAAYT-F--G  
NY---TVGLGYEKIDSP-----DTAL-----MADMEQLELAIAIAKFGATNVKAYYADGELDRDFARAV  
FDLTPVAAAATAVDHKAYGLSVDSTFGATTVGGYVQVLDIDTIDDVTVYYGLGASYDLGGGASIVGGIADNDL  
PNSDMVADLGVKFKF\* (SEQ ID NO:23)  
>P1;1osmA  
sequence: 1osmA : 10 : : 332 :  
KLDLYGKIDGLHYFSDDKDVD-GDQTYMRLGVKGETQINDQLTGYGQWEYNVQ-ANNTESSSDQAWTRLAFA  
GLKFGDAGSFDYGRNYGVVY-DVTSWTDVLPE-----FGGDTY-----GSDNFLQSRANGVATYRN-  
SDFFGLVDGLNFAHQY---QGKNGSVSSEGATNNRGAL---KQN-----GD---GFGTSVTYD-I--F  
D---GISAGFAYANS-----KRTDDQNQLLGEGLDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSL-  
-GFANKAQNFEVAAQYQFDGLRPSVAYLQSKGKDLNG-YGDQDILKYVDVGATYYFNKNMSTYVDYKINLL  
DDNSFTRSAGISTDD\* (SEQ ID NO:24)

**FIGURE 35**

P1;2mpr

structureX: 2mprA : 2 : : 427 : :

DFHGYARSGIGWTGS-----G---GEQQC-----FQA--TGAQSKYRLGNE-----  
--CETYAELKLGQEVWKEGDKSFYFDTNVAYSVNQOND--WEST-DPAFREANVQGKNL---IEWLPGSTIW  
AGKRFYQRHD---VHMIDFYYWDISGPGAGIENIDLGFGLS-LAATRSTEAGGSYTFSSQNIYDEVKDTAN  
DVFDVRLAGLQTNPDGVLELGVDYGRANTTDGYKL-ADGASKDGWMFTAETHQSMLKGYNKFVVQYATDAMT  
TQGKGQARGSDGSSFTEKINYANKVINNNG-NMWRILDHGAISLGDKWDLMYVGMYQNIWDNNL--GTEW  
WTGVVRPMYKWTPIMSTLLEVGYDNVKS-QQ-----TGDRNNQYKITLA-QQ---WQAGDSIWSRPAIRI  
FATYAKWDEKWKYIKGDNISRYAAAT-NSGISTNSRGDSDEWTFGAQMEIWW\* (SEQ ID NO:25)

>P1;1a0tP

sequence: 1a0tP : 4 : : 413 :

EFHGYARSGIVMNDGASTKSGAYITPAGETGG-----AIGRL-----GNQ-----  
--ADTYVEMNLEHKQTLDNGATTRFKVMVADGQTSYNDWTASTS-DLNVRQAFVELGNLPTFAGPFKGSTLW  
AGKRF--DRDNFDIHWIDSDVVFLAGTGGGIYDVWKWNDGLRSNFSLYGRNFGDIDDSNSVQNYILTMNHFA  
GPLQMMVSGLRAKDNDERKDSNG-NLAKGDAANTGV----HALLGLHNDSFYGLRDGSSKTALLYG-HGLG  
AEVKGIGSDGA-----LRPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQW  
ATFNRLIQAQNQNFALAYEGSYQYMD--LKPEGYNDRQAVNGSFYKLT--APTFKVGSIGDFFSRPEIRF  
YTSWMDWSKLNYYASDDALGS---DGF-----NSGGEWSFGVQMETWF\* (SEQ ID NO:26)

**FIGURE 37**